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1: pir1:*
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Gapop 10.0 ,
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3542
1 MAINTSNLCSLLFLLSLFLL.....SPRSTKQQQPLVSILDEVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length
  2001, 15:43:16; Search time 170.72 Seconds
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264.889 Million cell updates/sec
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globulin-2 precurs
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            vicilin precursor
canavalin - jack b
canavalin - sword
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A; Residues: 1-810 < YAM>
A; Cross references: EMBL: AB019195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 286;
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                                                   EQRSREDERRRHERQHCGRSRVNQVAIRRTEQEQSNNPYYFQEQRFQSRYRSDEGHWRVL
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S51941
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FWPMVA
T01662
T02258
T06572
S02281
T10443
S16334
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1198.5; DB 2;
Pred. No. 1.3e-67;
11; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g3808061; PIDN:BAA34056.1; PID:g3808062
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                                                                     -GEEEQSDNPYYFDERSLSTRFRTEEGHISVL
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globulin-1 - maize
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Gaps

23;

of a sin

31

195

93

65

227 292

273

Result

Minimum Maximum

DΒ DB

Database

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RESULT 2
$22477
vicilin precursor - cacao (cacao)
C;Species: Theobroma cacao (cacao)
C;Species: Theobroma cacao (cacao)
C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sqquence_revision 30-Sep-1993 #te
C;Accession: $22477; $22478; $18105; $22050
R;McHenry, L, Fritz, p.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nucleotide se
A;Title: Comparison of the structure and nucleotide se
A;Reference number: $22477
A;Reference number: $22477
A;Accession: $22477
A;Rolecule type: DNA
A;Residues: 1-566 <NCH>
A;Cross references: EMBU:X62625
A;Accession: $22478
A;Accession: $22478
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A:Introns: 211/1: 269/3: 296/3: 391/3: 502/1
C:Superfamily: glycinin
C:Keywords: seed: storage protein
F:1-24/Domain: signal sequence #status predicted
F:25-566/Product: vicilin #status predicted <MAT>
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A; Residues: 1-452 < MC2>
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mes 233; Conserv
IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL
                                                        LRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIR
                                                                                                           ER-GEHENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPP
                                                                                                                                                                                                                                                                          ICEEEEEYNR---QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
                                   LKGINDYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVS
                                                                                                                                             GRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL
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                                                                                                                                                                                                                    EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQHQCQLRCREQQRQH 223
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Pred. No. 4.5e
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A;Recession: S06398
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-globulin type A precursor - upland cotton W,Alternate names: seed storage protein C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1 C;Accession: S06398 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure
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                                                                                                                            EKYEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQ
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                                   LEANPNTFYLPHHCDAEKIYVYTNGRGTVTFVTHENKESYNVVPGVVVRIPAGSTVYLAN
                                                                   LEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLIN 353
                                                                                                                                                                                  NKWREEEEES-----
                                                                                                                                                                                                                                                        YEKQQQQQPDKQFKECQQRCQWQEQRPERKQQCVKECREQYQEDPWKGER
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                                                                                                                                                                                                                                                                                                                             Q--DKCEDRSETQLKEEQQRDGEDPQRRYQDCRQHCQQEERRLRP-----HCEQSCREQ
                                                                                                                                                                                                                                                                                                                                                               RCVSQCDKRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEE 113
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                                                                                                         ----DEGEQQQRNNPYYFHRRSFQERFREEHGNFRVLQRFADKHHLLRGINEFRIAI
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Pred. No. 4
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A;Status: not compared with conceptual transference.

A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.
C;Superfamily: glycinin
C;Reywords: glycoprotein; seed; storage protein
C;Reywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence **status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein *status predicted
F;417/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C;Species: Gossyplum hirsutum (upland cotton) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-J C;Accession: A30838; S06911
C;Accession: A30838; S06911
C;Accession: A30838; S06911
C;Accession: A30838; S06911
C;Accession: Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis and A;Reference number: A30838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375 A:Experimental source: var. Coker 201 R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 A:Title: Developmental biochemistry of cottonseed embryogenesis and germ A:Reference number: S06398
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A; Residues: 1-588 < CHL>
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                                                                YEDCRRRCEQQE--PRQQHQCQLRCREQQRQHGRGGDMMNPQR------GGSGRYEEGEE
                                                                                                                     -- RQQEERQRPQCQQRCLKRFEQEQQQ
                                                                                                                                             QRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQRE 193
                                                                                                                                                                                                                            EDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEEYNRQR--DPQQQYEQCQKHC 133
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                                        FQECQQHCHQQEQRPERKQQCVRECRERYQE---
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38.5%; Pr
tive 112;
                                                                                                                                                                                                                                                                                           Score 1082.5;
Pred. No. 1.6e
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$208059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: $08059
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
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Best Local
                                      413
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                                      FG-----
                                                                                               NRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGV
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FGGRQSRRRQQGQGMFRKASQEQIRALSQEATSPR----
                                                                        NQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTRSEQLDEL
                                                                                                                                                   TLEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLA
                                                                                                                                                                                                                                EEAEEEETEEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLS 141
                                                                                                                                                                                                                                                                       --- GSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLV 292
                                                                                                                                                                                                                                                                                                             -----SQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQE-----NPWRGERE
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                                    -QQREGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYS
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39.3%;
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Pred. No. 7.8e
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7.8e-57;
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EKSGE - - RFAFNLLSQTPRYS
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XIX

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A; Accession: A43642
A; Status: preliminary
A; Molecule type: protein
A; Residues: 87-100 < KRI>
C; Superfamily: glycinin
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C;Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A53234; A43642
R;Belanger, F.C.; Kriz, A.L.
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Biochem. Genet. 27, 239-251, 1989
A; Title: Characterization of embryo globulins A; Reference number: A43642; MUID: 89374022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Scaled Etype: DNA
A; Molecule type: DNA
A; Residues: 1-573 <BEL>
A; Experimental source: inbred line Va 26
A; Experimence extracted from NCBI backbone (NCBIN:71280,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism
A:Reference number: A53234; MUID:92090707
A;Accession: A53234
A;Status: preliminary
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                                     YGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPH
                                                                                                      FGQ--QREGVIIRASQEQIRELTRDDSE---SRHWHIRRGGESSRGPYNLFNKRPLYSNK 467
                                                                                                                                                                                                                                                                                  LLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLI 352
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HGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAEIVCPH
                                                                             FGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIANQ
                                                                                                                                                              NTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLERL
                                                                                                                                                                                                   NRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGV 412
                                                                                                                                                                                                                                           VLEANPRSFVVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTYLA 204
                                                                                                                                                                                                                                                                                                                          EDEREREQEKEEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYRVA 144
                                                                                                                                                                                                                                                                                                                                                 ----RYEEGEEEQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLV 292
                                                                                                                                                                                                                                                                                                                                                                                                     EDDNHHHHGGHKSGRCVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADDRSGEGSS 84
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Pred. No. 1.3e-49;
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A;Gene: Glb1-L
A;Introns: 167/1; 225/3;
C;Superfamily: glycinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Zea mays (maize)
C;Date: (02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C;Date: (02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: B53234; S21824
R;Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism of the maize G
A;Reference number: A53234; MUID:92090707
A;Accession: B53234
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A; Residues: 1-582 <BEL>
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                    NENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIF
                                                                                                                                                         LYEADARSFHDLAEHDVSVSFANITAGSMSAPLFNTRSFKIAYVPNGKGYAEIVCPHRQS
                                                                                                                                                                                 AYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVAASGEADVEMACPHLSG
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DSNLQTVCFEVHADRNEKVFLAGAD-NVLQKLDRVAKALSFASKAEEVDEVLGSRREKGF
                                                                            QGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVAVASR
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39.2%;
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RESULT 8
$35221
globulin Beg1 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
C;Accession: $35221
R;Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D.
Mol. Gen. Genet. 239, 209-218, 1993
Mol. Gen. Gen. Genet. 239, 209-218, 1993
Mol. Gen. Gen. Genet. 239, 2
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C:Superfamily: glycinin
C:Keywords: glycoprotein
F:174-190/Product: globulin Beg1 #status predicted <MAT>
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A; Residues: 1-637 <HEC>
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EESFNSQDQSI-FFPGPRQHQQQSPRSTKQQQ 655
                                                                      GHPVVEISSSQGSSNLQVVCFEINAERNERVWLAGR-NNVIGKLGSPAQELTFGRPAREV
                                                                                                                 GHPVVFVSS - - GNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEV
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A; Residues: 361-639 C; Genetics:
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C;Date: 07-Mar-1988 #sequence_revision 30
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R; Doyle, J.J.; Schuler, M.A.; Godette,
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J. Biol. Chem. 261, 9228-9238, 1986

A;Title: The glycosylated seed storage proteins of Glycine max a A;Reference number: A24810; MUID:86250867

A;Accession: B24810

A;Molecule type: DNA

A;Residues: 1-639 <DOY>
A;Cross-references: GB:M13759; NID:g169928; PIDN:AAB01374.1; PID A;Note: the authors translated the codon GGT for residue 352 as R;Schuler, M.A.; Schmitt, E.S.; Beachy, R.N.

Nucleic Acids Res. 10, 8225-8244, 1982

A;Title: Closely related families of genes code for the alpha an A;Reference number: S16337; MUID:83143288

A;Accession: S16337
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                         TKVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEED-VHYEQVRARLSKREAIVVLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                   DPQQ--QYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEE
                                                                           SSEDKPFNLGSRDPIYSNKLGKLFEITQRN-PQLRDLDVFLSVVDMNEGALFLPHFNSKA
                                                                                                                 ESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRS
                                                                                                                                                                                                                                      AALNTQTEKLRGVF-----GQQ-----REGVIIRASQEQIRELTRDDSESRHWHIRRGG
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                                                                                                                                                                                    ASYDTKFEEINKVLFGREEGQQQGEERLQESVIVEISKKQTRELSKHAKSSS---
                                                                                                                                                                                                                                                                                                                                          ----AGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE
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Pred. No. 2.6e-46;
Prematches 221;
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beta-conglycinin alpha chain precursor - soybean
C;Species; Glycine max (soybean)
C;Species; Glycine max (soybean)
C;Species; Glycine max (soybean)
C;Accession: S20007
R;Lelievre, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C.
Plant Mol. Biol. 18, 259-274, 1992
A;Fittle: Synthesis and assembly of soybean beta-conglycinin in vitro.
A;Reference number: S20007; MUID:92119248
A;Accession: S20007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-605 <LEL>
C;Superfamily: glycinin
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AQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSP
                                                          GRGGGK-----RHEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGIN
                                                                                         ITPEKNPQLRDLDIFLSIVDMNEGALLLPHFNSKAIVILVINEGDANIELV------
                                                                                                                     VKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHG
                                                                                                                                                                                                                LAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSREEGQQQGE
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                                                                                                                                                                                 QR--EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE 473
                                                                                                                                                                                                                                             FLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF------GQ
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30.6%; Pred. No. 1.86
tive 143; Mismatches
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A; Accession: S74124
A; Molecule type: protein
A; Residues: 189-196,'H',198,'N',200,'X',202-203;397-408,'X',410,'X',412-417,'X',419-4
A; Eszperimental source: seed
C; Superfamily: glycinin
C; Keywords: glycoprotein; seed; storage protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-62/Domain: signal sequence #status predicted <PRO>
F;63-605/Product: beta-conglycinin alpha chain #status predicted <MAT>
F;261,517/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Title: Limited proteolysis of beta-conglycinin and A;Reference number: S74123; MUID:97054613
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A;Title: Complete sequence of a cDNA of alpha A;Reference number: S14681; MUID:91355860
A;Accession: S14681
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A; Residues: 1-605 <SEB>
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                                                  QR--EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE 473
                                                                                                     LAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSREEGQQQGE 368
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                                                                                                                                                        FLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF-----
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Pred. No. 2.4e-45;
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R;Bown, D.; Ellis, T H.N.; Gatehouse, J.A.

Biochem. J. 251, 717-726, 1988

A;Title: The sequence of a gene encoding convicilin from the sequence of a gene encoding convicilin from the sequence of a gene encoding convicilin from the sequence of the sequence of the sequence of the sequence of the sequence, including the amino end of the sequence of this sequence, including the amino end of the sequence of the se
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c;Species: pisum sativum (garden pea)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C;Accession: S00566
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A;Title: A 62-kD sucrose binding protein is expressed and localized A;Reference number: JQ1730; MUID:93104680
A;Accession: JQ1730
A;Molecule type: mRNA
A;Residues: 1-524 <GRI>
A;Cross-references: GB:L06038; NID:91431744; PIDN:AAB03894.1; PID:91
C;Superfamily: glyclinin
C;Keywords: sugar transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 33.9 ues 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
KRPLYSNKYGQAYEVKPEDYRQ--LQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVVASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KQIQEETREKKEE-ESREREE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.8%; Score 808; DB 2; 33.9%; Pred. No. 2.2e-43; cive 97; Mismatches 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662
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273 FAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPG-PR GRHGGRGGGKRHEEEE-----DVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLL LFEITPEKKYPQLQDLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLELL-----AYEVKPE-DYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLS ----GQQREGVIIRASQEQIRELTRDDSESRHWHTRRGGESSRGPYNLFNKRPLYSNKYGQ NRPGKFEAF - - GLSENKNQYLRGFSKNILEASLNTKYETIEKVLLEEQEKKPQQLRDRKR -GFGINAKNNQRNFLSGSDDNVISQIENPVKELTFPGSSQEVNRLIKNQKQSHFASAEPE -----GLKNEQQEREDRKERNNEVQRYEARLSPGDVVIIPAGHPVAISASSNLNLL-TQQGEERD-AIIKVSREQIEELRKLAKSSS----KKSLPSEFEPFNLRSHKPEYSNKFGK 641 491 582 385 440 529

62K sucrose-binding protein precursor - soybean c;Species: Glycine max (soybean) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999 C;Accession: JQ1730 localized in tissues active PID: 9170064 W.D.

AALNTQTEKLRGVFGQQREGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFN 459 RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE RCKEICEEEEEYNRQRDPQ--QQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQ 162 AALQTPKGKLENVFDQQNEGSIFRISREQVRALA-PTKKSSWWPF--GGE-SKPQFNIFS HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ LLQGIENFRLAILEARAHTFVSPRHFDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMI 200 LLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVI KCKETEVEEE-----DPELVTCKHQCQQQQQYTEGDKR---VCLQSCD-RYHRMKQERE HGRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSK KRYEEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQ Length 524; Indels Gaps 517 341 140 281 316 260 399 222 76 101 17;

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submitted to the EMBL Data Library, February 1997
A; Reference number: 215693
A; Accession: T06459
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-483 < ROD>
A; Cross-references: EMBL:Y11207; PIDN:CAA72090.1
A; Experimental source: var. Lincoln
C; Genetics:
A; Note: p54
C; Superfamily: glycinin
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N;Alternate names: P54 protein
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06459
R;Rodrigo II, M.I.
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Best Local Similarity
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   QAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQ 646
                                                            LANITKGSMSTIHYNTNANKIALVIDGEGELEMACPHMPS----SSSNSRQKKSSISYH
                                     NINAKLRPGVMFVVPAGHPFVNIASKKKNLIVVCFEVNAQRNKKLALAGK-KNIVSALDK
                                                                                                                                               IANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEEEDVHYE
                                                                                                                                                                                   LAPKKS----LWPF----GGPFKSPFNIFSNNPAFSNKFGSLFEVGPSQEKSGLEGLNLMLT
                                                                                                                                                                                                           LTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQDMDLSVF
                                                                                                                                                                                                                                                          PVNLEPFFESAGRKPESYLNTFSSKVLQAALKSSKGELETVLDEQKKGRIFKIEKEDVRG
                                                                                                                                                                                                                                                                               PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRASQEQIRE 431
                                                                                                                                                                                                                                                                                                                                  NIKGRGIIGLVAEDRTERFNLEEGDIMRVPAGTPMYLVNRDENEKLYIAAFHMPPSSGSA
                                                                                                                                                                                                                                                                                                                                                     VIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF---LQTIST 371
                                                                                                                                                                                                                                                                                                                                                                                                        EDNDFETKIDTKDGRVLILNKFNEKSKLLKNIENYGLAVLEIKANAFLSPHHYDSEAILF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RICMERCODYIKKKQE-----RQKHKEH------EEEEEQEQEEDENPYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQSDNPYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQREY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLDADAILL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKEKDP-ELTTCKDQCD-----MQRQYDEEDK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%; Score 769.5; DB 2; 31.4%; Pred. No. 5.2e-41; ative 114; Mismatches 169;
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Job time: 538 sec

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2001, 15:52:14

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RESULT 15
$24756
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$24756
vicilin-like storage protein precursor - white spruce
C;Species: Picca glauca (white spruce)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: $24756; $18873
R;Newton, C.H.; Filin, B.S.; Sutton, B.C.S.
Plant Mol. Biol. 20, 315-322, 1992
A;Title: Vicilin-like seed storage proteins in the gymnosperm interior spruce (FA;Reference number: $24756; MUID:93004485
A;Accession: $24756
A;Accession: $24756
A;Molecule type: mRNA
A;Residues: 1-448 <NEW>
A;Cross-references: EMBL:X63191; NID:920500; PIDN:CAA44873.1; PID:920501
C;Superfamily: vicilin
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                                                                                                                                                                                                                                                YSNKYGQAYEVKPEDYRQLQDMDLSVFTANVTQGSMMGPFFNTRSTKVVVVASGEADVEM
                                                                                                                                                                                                                                                                                                                           GVFGQQREGVIIRASQEQIRELTRDDSESRHWHIRRG---GESSR----GPYNLENKRPL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYL
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                                 HQQQSPRST
                                                                                                             AFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPR-KEVEESFNSQDQSIFFPGPRQ 642
                                                                                                                                                                                    ACPHLSGRHGGRGGGKRHEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLF
                                                                                                                                                                                                                            FENENGRETTAGPKNYPFLDALDVSVGLADLNPGSMTAPSLNSKSTSIGIVTNGEGRIEM
                                                                                                                                                                                                                                                                                                                                                                                 VNNDDHNTLRIASLVRPVSTVRGEYQPFYVAGGRNPQTVYSAFSDDVLEAAFNTNVQQLE
                                                                                                                                                                                                                                                                                                                                                                                                   INRDNNERLHIAKFLQTIST-PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLR 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCIEMKPNTVMLPHYIDATWILYVTRGRGYIAYVHQNELVKRKLEEGDVFGVPSGHTFYL
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RSRDEARSS
                                                                       WFDLNTRGNERQFLAGK-NNVLNTLEREIRQLSFNVPRGEEIEEVLQAQKDQVILRGPQR
                                                                                                                                                ACPHL-GQHG--WSSPRERGDQDITYQRVWAKLRTGSVYIVPAGHPITEIASTNSRLQIL
                                                                                                                                                                                                                                                                                                     RIFGGHKSGVIIHANEEQIREMMR------KRGFSAGSMSAPEHPKPFNLRNQKPD
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447
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Pred. No. 5.9e-40;
5; Mismatches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 448;
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